

FIG. 1



1	56
Il6 human	MnsFStsaFgPVAFsLGLLLVlpaAFPapvpggeDskDvaaPhrQpLTsSErIDkg
Il6 mouse	MkFLSaRdFhPVAF.LGLMLVttTAFPTsqvrRGDFtEdttPnRpVyTtSQ.VGg1
Il6 hhv8	McWFklwsL...L1VGsLLVsgt.....RGKLpDapefeKDLLi.....qr
Consensus	* **
57	112
Il6 human	IrYILdgIsaLRKEtCNKsnMCeSSkeALAEENNlNlPkMaEkDGCfQsGFNEEtCL
Il6 mouse	IthVLWeiVEMRKELCNgnSdCmndDALAEENNlKLPeIgrnDGCYQtGYNQEIcL
Il6 hhv8	LnWMLWvidEcfrDLcYrtGICKGilePaaifhLKLPaInDtDhCgliGFNEtsCL
Consensus	* * * * * ^ ^
113	168
Il6 human	VKIitGLLEFEFVLEYLqNrF.EsSeEqARaVQMstKvLIQFLQkkaKNLdaIttP
Il6 mouse	LKIssGLLEYhsYLEYmKnNlKdnkkDkARVLQrdTeTLIHIFnQEVKDLhKivlP
Il6 hhv8	kKLadGFFEFELVlfkFLtteF.GkSvinvdVMELlTKTLgwdIQEELnklLtKthys
Consensus	* * * * * ^
169	223
Il6 human	dPttnASLLtKLQAQnQWLqdmTtHLILRSFkEFLqssLRaLRQM.....
Il6 mouse	tPisNALltDKLESQKEWLRtkTiQfILKSLEEFkvtLRstrQt.....
Il6 hhv8	pPkfDrGLLGRLQGLKyWVRhfafYVLsAMEkFaggavRvLdsIpdvtvpdvhdK
Consensus	* * * * * ^



FIG. 2A

SEQUENCE LISTING

1. Sequence characteristics:
 - 1.1. Length: 612 base pairs
 - 1.2. Type: Nucleic Acid
 - 1.3. Strandedness: Double stranded
 - 1.4. Topology: Linear
2. Molecule type: Genomic DNA
3. Description: Human herpesvirus 8 interleukin-6 gene
4. Hypothetical: No
5. Anti-sense: No
6. Original source: Kaposi Sarkoma from HIV positive donor
7. Organism: Human herpesvirus 8

FIG. 2 B

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1  ATG TGC TGG TTC AAG TTG TGG TCT CTC TTG CTG GTC GGT TCA CTG
1  M   C   W   F   K   L   W   S   L   L   L   V   G   S   L
1  Met Cys Trp Phe Lys Leu Trp Seu Leu Leu Leu Val Gly Ser Leu

46 CTG GTA TCT GGA ACG CGG GGC AAG TTG CCG GAC GCC CCC GAG TTT
16  L   V   S   G   T   R   G   K   L   P   D   A   P   E   F
16  Leu Val Ser Gly Thr Arg Gly Lys Leu Pro Asp Ala Pro Glu Phe

91  GAA AAG GAT CTT CTC ATT CAG AGA CTC AAT TGG ATG CTA TGG GTG
31  E   K   K   L   L   I   Q   R   L   N   W   M   L   W   V
31  Glu Lys Asp Leu Leu Ile Gln Arg Leu Asn Trp Met Leu Trp Val

136 ATC GAT GAA TGC TTC CGC GAC CTC TGT TAC CGT ACC GGC ATC TGC
46  I   D   E   C   F   R   D   L   C   Y   R   T   G   I   C
46  Ile Asp Glu Cys Phe Arg Asp Leu Cys Tyr Arg Thr Gly Ile Cys

181 AAG GGT ATT CTA GAG CCC GCT GCT ATT TTT CAT CTG AAA CTA CCA
61  K   G   I   L   E   P   A   A   I   F   H   L   K   L   P
61  Lys Gly Ile Leu Glu Pro Ala Ala Ile Phe His Leu Lys Leu Pro

226 GCC ATC AAC GAT ACT GAT CAC TGC GGG TTA ATA GGA TTT AAT GAG
76  A   I   N   D   T   D   H   C   G   L   I   G   F   N   E
76  Ala Ile Asn Asp Thr Asp His Cys Gly Leu Ile Gly Phe Asn Glu

271 ACT AGC TGC CTT AAA AAG CTC GCC GAT GGC TTT TTT GAA TTC GAG
91  T   S   C   L   K   K   L   A   D   G   F   F   E   F   E
91  Thr Ser Cys Leu Lys Lys Leu Ala Asp Gly Phe Phe Glu Phe Glu

316 GTG TTG TTT AAG TTT TTA ACG ACG GAG TTT GGA AAA TCA GTG ATA
106 V   L   F   K   F   L   T   T   E   F   G   K   S   V   I
106 Val Leu Phe Lys Phe Leu Thr Thr Glu Phe Gly Lys Ser Val Ile

361 AAC GTG GAC GTC ATG GAG CTT CTG ACG AAG ACC TTA GGA TGG GAC
121 N   V   D   V   M   E   L   L   T   K   T   L   G   W   D
121 Asn Val Asp Val Met Glu Leu Leu Thr Lys Thr Leu Gly Trp Asp

406 ATA CAG GAA GAG CTC AAT AAG CTG ACT AAG ACG CAC TAC AGT CCA
136 I   Q   E   E   L   N   K   L   T   K   T   H   Y   S   P
136 Ile Gln Glu Glu Leu Asn Lys Leu Thr Lys Thr His Tyr Ser Pro

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FIG. 2C

451	CCC	AAA	TTT	GAC	CGC	GGT	CTA	TTA	GGG	AGG	CTT	CAG	GGA	CTT	AAG
151	P	K	F	D	R	G	L	L	G	R	L	Q	G	L	K
151	Pro	Lys	Phe	Asp	Arg	Gly	Leu	Leu	Gly	Arg	Leu	Gln	Gly	Leu	Lys
496	TAT	TGG	GTG	AGA	CAC	TTT	GCT	TCG	TTT	TAT	GTT	CTG	AGT	GCA	ATG
166	Y	W	V	R	H	F	A	S	F	Y	V	L	S	A	M
166	Tyr	Trp	Val	Arg	His	Phe	Ala	Ser	Phe	Tyr	Val	Leu	Ser	Ala	Met
541	GAA	AAG	TTT	GCA	GGT	CAA	GCG	GTG	CGT	GTT	TTG	GAC	TCT	ATC	CCA
181	E	K	F	A	G	Q	A	V	R	V	L	D	S	I	P
181	Glu	Lys	Phe	Ala	Gly	Gln	Ala	Val	Arg	Val	Leu	Asp	Ser	Ile	Pro
586	GAC	GTG	ACT	CCT	GAC	GTC	CAC	GAT	AAG						
196	D	V	T	P	D	V	H	D	K						
196	Asp	Val	Thr	Pro	Asp	Val	His	Asp	Lys						